



#6

1

SEQUENCE LISTING

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RIOUX, STEPHANE
BRODEUR, BERNARD R.
HAMEL, JOSEE
RHEAULT, PATRICK

<120> STREPTOCOCCUS PYOGENES POLYPEPTIDES AND CORRESPONDING
DNA FRAGMENTS

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<141> 2002-02-21

<150> 60/269,840

<151> 2001-02-21

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<170> PatentIn Ver. 2.1

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<212> PRT

<213> Streptococcus pyogenes

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Val Asp Asp Thr Val Thr Asp Leu Phe Ser Asp Lys Arg Thr Thr Pro
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Glu Lys Ile Lys Asp Asn Leu Ala Lys Gly Pro Arg Glu Gln Glu Leu
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Lys Ala Val Thr Glu Asn Thr Glu Ser Glu Lys Gln Ile Thr Ser Gly
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Gln	Val	Ala	Ser	Phe	Ala	Phe	Thr	Pro	Asp	Lys	Lys	Thr	Ala	Ile	Ala	180	185		190
Glu	Tyr	Thr	Ser	Arg	Ala	Gly	Glu	Asn	Gly	Glu	Ile	Ser	Gln	Leu	Asp	195	200		205
Val	Asp	Gly	Lys	Glu	Ile	Ile	Asn	Glu	Gly	Glu	Val	Phe	Asn	Ser	Tyr	210	215		220
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Phe	Asp	Asn	Gln	Ile	Thr	Gly	Lys	Leu	Ser	Leu	Pro	Arg	Gln	Leu	Met	290	295		300
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Asn	Asp	Leu	Ser	Gln	Leu	Met	Leu	Pro	Asp	Gly	Leu	Glu	Lys	Ile	Glu	340	345		350
Ser	Glu	Ala	Phe	Thr	Gly	Asn	Pro	Gly	Asp	Asp	His	Tyr	Asn	Asn	Arg	355	360		365
Val	Val	Leu	Trp	Thr	Lys	Ser	Gly	Lys	Asn	Pro	Ser	Gly	Leu	Ala	Thr	370	375		380
Glu	Asn	Thr	Tyr	Val	Asn	Pro	Asp	Lys	Ser	Leu	Trp	Gln	Glu	Ser	Pro	385	390		400
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 Ala Ser Asp Asp Leu Glu Glu Ile Lys Glu Gly Ala Phe Met Asn Asn
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 Arg Ile Glu Thr Leu Glu Leu Lys Asp Lys Leu Val Thr Ile Gly Asp
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 Ala Ala Phe His Ile Asn His Ile Tyr Ala Ile Val Leu Pro Glu Ser
 530 535 540
 Val Gln Glu Ile Gly Arg Ser Ala Phe Arg Gln Asn Gly Ala Asn Asn
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 Thr Glu Ile Pro Val Gln Ala Phe Ser Asp Asn Ala Leu Lys Glu Val
 595 600 605
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 Asn His Leu Lys Gln Leu Glu Val Ala Ser Ala Leu Ser His Ile Ala
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 Phe Asn Ala Leu Asp Asp Asn Asp Gly Asp Glu Gln Phe Asp Asn Lys
 645 650 655
 Val Val Val Lys Thr His His Asn Ser Tyr Ala Leu Ala Asp Gly Glu
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 675 680 685
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 Ser Ala Ile Lys Lys Ala Asn Val Lys Arg Leu Glu Lys Glu Leu Asp
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 Leu Leu Thr Gly Leu Val Glu Gly Lys Gly Pro Leu Ala Gln Ala Thr
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 820 825 830
 Tyr Tyr Ile Gly Leu Asn Val Tyr Phe Asp Lys Ser Gly Lys Leu Ile
 835 840 845
 Tyr Ala Leu Asp Met Ser Asp Thr Ile Gly Glu Gly Gln Lys Asp Ala
 850 855 860
 Tyr Gly Asn Pro Ile Leu Asn Val Asp Glu Asp Asn Glu Gly Tyr His
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 Thr Ile Leu Asn Ser Lys Leu Ser Gln Leu Thr Ser Ile Arg Gln Val
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 Pro Thr Ala Ala Tyr His Arg Ala Gly Ile Phe Gln Ala Ile Gln Asn
 915 920 925
 Ala Ala Ala Glu Ala Glu Gln Leu Leu Pro Lys Pro Gly Thr His Ser
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 Glu Lys Ser Ser Ser Ser Glu Ser Ala Asn Ser Lys Asp Arg Gly Leu
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<213> Streptococcus pyogenes

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Arg	Gln	Val	Pro	Thr	Ala	Ala	Tyr	His	Arg	Ala	Gly	Ile	Phe	Gln	Ala	865	870	875	880
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Thr	His	Ser	Glu	Lys	Ser	Ser	Ser	Ser	Glu	Ser	Ala	Asn	Ser	Lys	Asp	900	905	910	
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<212> PRT

<213> Streptococcus pyogenes

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Asp Lys Arg Thr Thr Pro Glu Lys Ile Lys Asp Asn Leu Ala Lys Gly
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Pro Arg Glu Gln Glu Leu Lys Ala Val Thr Glu Asn Thr Glu Ser Glu
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Lys Gln Ile Asn Ser Gly Ser Gln Leu Glu Gln Ser Lys Glu Ser Leu
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Ser Leu Asn Lys Arg Val Pro Ser Thr Ser Asn Trp Glu Ile Cys Asp
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Phe Ile Thr Lys Gly Asn Thr Leu Val Gly Leu Ser Lys Ser Gly Val
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Asp Gly Thr Gln Leu Ile Gln Val Ala Ser Phe Ala Phe Thr Pro Asp
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Lys Lys Thr Ala Ile Ala Glu Tyr Thr Ser Arg Ala Gly Glu Asn Gly
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Glu Ile Ser Gln Leu Asp Val Asp Gly Lys Glu Ile Ile Asn Glu Gly
 180 185 190

Glu Val Phe Asn Ser Tyr Leu Leu Lys Lys Val Thr Ile Pro Thr Gly
 195 200 205

Tyr Lys His Ile Gly Gln Asp Ala Phe Val Asp Asn Lys Asn Ile Ala
 210 215 220

Glu Val Asn Leu Pro Glu Ser Leu Glu Thr Ile Ser Asp Tyr Ala Phe
 225 230 235 240

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Leu	Pro	Arg	Gln	Leu	Met	Arg	Leu	Ala	Glu	Arg	Ala	Phe	Lys	Ser	Asn	275	280	285
His	Ile	Lys	Thr	Ile	Glu	Phe	Arg	Gly	Asn	Ser	Leu	Lys	Val	Ile	Gly	290	295	300
Glu	Ala	Ser	Phe	Gln	Asp	Asn	Asp	Leu	Ser	Gln	Leu	Met	Leu	Pro	Asp	305	310	315
Gly	Leu	Glu	Lys	Ile	Glu	Ser	Glu	Ala	Phe	Thr	Gly	Asn	Pro	Gly	Asp	325	330	335
Asp	His	Tyr	Asn	Asn	Arg	Val	Val	Leu	Trp	Thr	Lys	Ser	Gly	Lys	Asn	340	345	350
Pro	Tyr	Gly	Leu	Ala	Thr	Glu	Asn	Thr	Tyr	Val	Asn	Pro	Asp	Lys	Ser	355	360	365
Leu	Trp	Gln	Glu	Ser	Pro	Glu	Ile	Asp	Tyr	Thr	Lys	Trp	Leu	Glu	Glu	370	375	380
Asp	Phe	Thr	Tyr	Gln	Lys	Asn	Ser	Val	Thr	Gly	Phe	Ser	Ser	Lys	Gly	385	390	395
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Asp	Phe	Gln	Asn	Lys	Thr	Leu	Arg	Lys	Tyr	Asp	Leu	Glu	Glu	Val	Lys	435	440	445
Leu	Pro	Ser	Thr	Ile	Arg	Lys	Ile	Gly	Ala	Phe	Ala	Phe	Gln	Ser	Asn	450	455	460
Asn	Leu	Lys	Ser	Phe	Glu	Ala	Ser	Asp	Asp	Leu	Glu	Glu	Ile	Lys	Glu	465	470	475
Gly	Ala	Phe	Met	Asn	Asn	Arg	Ile	Glu	Thr	Leu	Glu	Leu	Lys	Asp	Lys	485	490	495
Leu	Val	Thr	Ile	Gly	Asp	Ala	Ala	Phe	His	Ile	Asn	His	Ile	Tyr	Ala	500	505	510
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Glu	Gln	Phe	Asp	Asn	Lys	Val	Val	Val	Lys	Thr	His	His	Asn	Ser	Tyr	625	630	635	640
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Ser	Thr	Ile	Val	Asp	Leu	Glu	Lys	Ile	Leu	Lys	Leu	Ile	Glu	Gly	Leu	660	665	670	
Asp	Tyr	Ser	Thr	Leu	Arg	Gln	Thr	Thr	Gln	Thr	Gln	Phe	Arg	Asp	Met	675	680	685	
Thr	Thr	Ala	Gly	Lys	Ala	Leu	Leu	Ser	Lys	Ser	Asn	Leu	Arg	Gln	Gly	690	695	700	
Glu	Lys	Gln	Lys	Phe	Leu	Gln	Glu	Ala	Gln	Phe	Phe	Leu	Gly	Arg	Val	705	710	715	720
Asp	Leu	Asp	Lys	Ala	Ile	Ala	Lys	Ala	Glu	Lys	Ala	Leu	Val	Thr	Lys	725	730	735	
Lys	Ala	Thr	Lys	Asn	Gly	Gln	Leu	Leu	Glu	Arg	Ser	Ile	Asn	Lys	Ala	740	745	750	
Val	Leu	Ala	Tyr	Asn	Asn	Ser	Ala	Ile	Lys	Lys	Ala	Asn	Val	Lys	Arg	755	760	765	
Leu	Glu	Lys	Glu	Leu	Asp	Leu	Leu	Thr	Gly	Leu	Val	Glu	Gly	Lys	Gly	770	775	780	
Pro	Leu	Ala	Gln	Ala	Thr	Met	Val	Gln	Gly	Val	Tyr	Leu	Leu	Lys	Thr	785	790	795	800
Pro	Leu	Pro	Leu	Pro	Glu	Tyr	Tyr	Ile	Gly	Leu	Asn	Val	Tyr	Phe	Asp	805	810	815	
Lys	Ser	Gly	Lys	Leu	Ile	Tyr	Ala	Leu	Asp	Met	Ser	Asp	Thr	Ile	Gly	820	825	830	
Glu	Gly	Gln	Lys	Asp	Ala	Tyr	Gly	Asn	Pro	Ile	Leu	Asn	Val	Asp	Glu	835	840	845	

Asp Asn Glu Gly Tyr His Ala Leu Ala Val Ala Thr Leu Ala Asp Tyr
 850 855 860
 Glu Gly Leu Asp Ile Lys Thr Ile Leu Asn Ser Lys Leu Ser Gln Leu
 865 870 875 880
 Thr Ser Ile Arg Gln Val Pro Thr Ala Ala Tyr His Arg Ala Gly Ile
 885 890 895
 Phe Gln Ala Ile Gln Asn Ala Ala Ala Glu Ala Glu Gln Leu Leu Pro
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 Lys Ala Gly Thr His Ser Glu Lys Ser Ser Ser Ser Glu Ser Ala Asn
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 Ser Lys Asp Arg Gly Leu Gln Ser Asn Pro Lys Thr Asn Arg Gly Arg
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 Gly Ile Leu Gly Tyr Thr Ser Val Ala Leu
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 Lys Ile Lys Asp Asn Leu Ala Lys Gly Pro Arg Glu Gln Glu Leu Lys
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 Ala Val Thr Glu Asn Thr Glu Ser Glu Lys Gln Ile Asn Ser Gly Ser
 65 70 75 80
 Gln Leu Glu Gln Ser Lys Glu Ser Leu Ser Leu Asn Lys Arg Val Pro
 85 90 95
 Ser Thr Ser Asn Trp Glu Ile Cys Asp Phe Ile Thr Lys Gly Asn Thr
 100 105 110
 Leu Val Gly Leu Ser Lys Ser Gly Val Glu Lys Leu Ser Gln Thr Asp
 115 120 125
 His Leu Val Leu Pro Ser Gln Ala Ala Asp Gly Thr Gln Leu Ile Gln
 130 135 140

Val	Ala	Ser	Phe	Ala	Phe	Thr	Pro	Asp	Lys	Lys	Thr	Ala	Ile	Ala	Glu	145	150	155	160
Tyr	Thr	Ser	Arg	Ala	Gly	Glu	Asn	Gly	Glu	Ile	Ser	Gln	Leu	Asp	Val	165	170	175	
Asp	Gly	Lys	Glu	Ile	Ile	Asn	Glu	Gly	Glu	Val	Phe	Asn	Ser	Tyr	Leu	180	185	190	
Leu	Lys	Lys	Val	Thr	Ile	Pro	Thr	Gly	Tyr	Lys	His	Ile	Gly	Gln	Asp	195	200	205	
Ala	Phe	Val	Asp	Asn	Lys	Asn	Ile	Ala	Glu	Val	Asn	Leu	Pro	Glu	Ser	210	215	220	
Leu	Glu	Thr	Ile	Ser	Asp	Tyr	Ala	Phe	Ala	His	Leu	Ala	Leu	Lys	Gln	225	230	235	240
Ile	Asp	Leu	Pro	Asp	Asn	Leu	Lys	Ala	Ile	Gly	Glu	Leu	Ala	Phe	Phe	245	250	255	
Asp	Asn	Gln	Ile	Thr	Gly	Lys	Leu	Ser	Leu	Pro	Arg	Gln	Leu	Met	Arg	260	265	270	
Leu	Ala	Glu	Arg	Ala	Phe	Lys	Ser	Asn	His	Ile	Lys	Thr	Ile	Glu	Phe	275	280	285	
Arg	Gly	Asn	Ser	Leu	Lys	Val	Ile	Gly	Glu	Ala	Ser	Phe	Gln	Asp	Asn	290	295	300	
Asp	Leu	Ser	Gln	Leu	Met	Leu	Pro	Asp	Gly	Leu	Glu	Lys	Ile	Glu	Ser	305	310	315	320
Glu	Ala	Phe	Thr	Gly	Asn	Pro	Gly	Asp	Asp	His	Tyr	Asn	Asn	Arg	Val	325	330	335	
Val	Leu	Trp	Thr	Lys	Ser	Gly	Lys	Asn	Pro	Tyr	Gly	Leu	Ala	Thr	Glu	340	345	350	
Asn	Thr	Tyr	Val	Asn	Pro	Asp	Lys	Ser	Leu	Trp	Gln	Glu	Ser	Pro	Glu	355	360	365	
Ile	Asp	Tyr	Thr	Lys	Trp	Leu	Glu	Glu	Asp	Phe	Thr	Tyr	Gln	Lys	Asn	370	375	380	
Ser	Val	Thr	Gly	Phe	Ser	Ser	Lys	Gly	Leu	Gln	Lys	Val	Lys	Arg	Asn	385	390	395	400
Lys	Asn	Leu	Glu	Ile	Pro	Lys	Gln	His	Asn	Gly	Val	Thr	Ile	Thr	Glu	405	410	415	
Ile	Gly	Asp	Asn	Ala	Phe	Arg	Asn	Val	Asn	Phe	Gln	Asn	Lys	Thr	Leu	420	425	430	
Arg	Lys	Tyr	Asp	Leu	Glu	Glu	Val	Lys	Leu	Pro	Ser	Thr	Ile	Arg	Lys	435	440	445	

Ile	Gly	Ala	Phe	Ala	Phe	Gln	Ser	Asn	Asn	Leu	Lys	Ser	Phe	Glu	Ala	450	455	460
Ser	Asp	Asp	Leu	Glu	Glu	Ile	Lys	Glu	Gly	Ala	Phe	Met	Asn	Asn	Arg	465	470	475
Ile	Glu	Thr	Leu	Glu	Leu	Lys	Asp	Lys	Leu	Val	Thr	Ile	Gly	Asp	Ala	485	490	495
Ala	Phe	His	Ile	Asn	His	Ile	Tyr	Ala	Ile	Val	Leu	Pro	Glu	Ser	Val	500	505	510
Gln	Glu	Ile	Gly	Arg	Ser	Ala	Phe	Arg	Gln	Asn	Gly	Ala	Asn	Asn	Leu	515	520	525
Ile	Phe	Met	Gly	Ser	Lys	Val	Lys	Thr	Leu	Gly	Glu	Met	Ala	Phe	Leu	530	535	540
Ser	Asn	Arg	Leu	Glu	His	Leu	Asp	Leu	Ser	Glu	Gln	Lys	Gln	Leu	Thr	545	550	555
Glu	Ile	Pro	Val	Gln	Ala	Phe	Ser	Asp	Asn	Ala	Leu	Lys	Glu	Val	Leu	565	570	575
Leu	Pro	Ala	Ser	Leu	Lys	Thr	Ile	Arg	Glu	Glu	Ala	Phe	Lys	Lys	Asn	580	585	590
His	Leu	Lys	Gln	Leu	Glu	Val	Ala	Ser	Ala	Leu	Ser	His	Ile	Ala	Phe	595	600	605
Asn	Ala	Leu	Asp	Asp	Asn	Asp	Gly	Asp	Glu	Gln	Phe	Asp	Asn	Lys	Val	610	615	620
Val	Val	Lys	Thr	His	His	Asn	Ser	Tyr	Ala	Leu	Ala	Asp	Gly	Glu	His	625	630	635
Phe	Ile	Val	Asp	Pro	Asp	Lys	Leu	Ser	Ser	Thr	Ile	Val	Asp	Leu	Glu	645	650	655
Lys	Ile	Leu	Lys	Leu	Ile	Glu	Gly	Leu	Asp	Tyr	Ser	Thr	Leu	Arg	Gln	660	665	670
Thr	Thr	Gln	Thr	Gln	Phe	Arg	Asp	Met	Thr	Thr	Ala	Gly	Lys	Ala	Leu	675	680	685
Leu	Ser	Lys	Ser	Asn	Leu	Arg	Gln	Gly	Glu	Lys	Gln	Lys	Phe	Leu	Gln	690	695	700
Glu	Ala	Gln	Phe	Phe	Leu	Gly	Arg	Val	Asp	Leu	Asp	Lys	Ala	Ile	Ala	705	710	715
Lys	Ala	Glu	Lys	Ala	Leu	Val	Thr	Lys	Lys	Ala	Thr	Lys	Asn	Gly	Gln	725	730	735
Leu	Leu	Glu	Arg	Ser	Ile	Asn	Lys	Ala	Val	Ser	Ala	Tyr	Asn	Asn	Ser	740	745	750

Ala Ile Lys Lys Ala Asn Val Lys Arg Leu Glu Lys Glu Leu Asp Leu
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 Leu Thr Gly Leu Val Glu Gly Lys Gly Pro Leu Ala Gln Ala Thr Met
 770 775 780
 Val Gln Gly Val Tyr Leu Leu Lys Thr Pro Leu Pro Leu Pro Glu Tyr
 785 790 795 800
 Tyr Ile Gly Leu Asn Val Tyr Phe Asp Lys Ser Gly Lys Leu Ile Tyr
 805 810 815
 Ala Leu Asp Met Ser Asp Thr Ile Gly Glu Gly Gln Lys Asp Ala Tyr
 820 825 830
 Gly Asn Pro Ile Leu Asn Val Asp Glu Asp Asn Glu Gly Tyr His Ala
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 Leu Ala Val Ala Thr Leu Ala Asp Tyr Glu Gly Leu Asp Ile Lys Thr
 850 855 860
 Ile Leu Asn Ser Lys Leu Ser Gln Leu Thr Ser Ile Arg Gln Val Pro
 865 870 875 880
 Thr Ala Ala Tyr His Arg Ala Gly Ile Phe Gln Ala Ile Gln Asn Ala
 885 890 895
 Ala Ala Glu Ala Glu Gln Leu Leu Pro Lys Pro Gly Thr His Ser Glu
 900 905 910
 Lys Ser Ser Ser Ser Glu Ser Ala Asn Ser Lys Asp Arg Gly Leu Gln
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 Ser Asn Pro Lys Thr Asn Arg Gly Arg His Ser Ala Ile Leu Pro Arg
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Asp	Lys	Arg	Thr	Thr	Pro	Glu	Lys	Ile	Lys	Asp	Asn	Leu	Ala	Lys	Gly	50	55	60
Pro	Arg	Glu	Gln	Glu	Leu	Lys	Thr	Val	Thr	Glu	Asn	Thr	Glu	Ser	Glu	65	70	75
Lys	Gln	Ile	Thr	Ser	Gly	Ser	Gln	Leu	Glu	Gln	Ser	Lys	Glu	Ser	Leu	85	90	95
Ser	Leu	Asn	Lys	Thr	Val	Pro	Ser	Thr	Ser	Asn	Trp	Glu	Ile	Cys	Asp	100	105	110
Phe	Ile	Thr	Lys	Gly	Asn	Thr	Leu	Val	Gly	Leu	Ser	Lys	Ser	Gly	Val	115	120	125
Glu	Lys	Leu	Ser	Gln	Thr	Asp	His	Leu	Val	Leu	Pro	Ser	Gln	Ala	Ala	130	135	140
Asp	Gly	Thr	Gln	Leu	Ile	Gln	Val	Ala	Ser	Phe	Ala	Phe	Thr	Pro	Asp	145	150	155
Lys	Lys	Thr	Ala	Ile	Ala	Glu	Tyr	Thr	Ser	Arg	Ala	Gly	Glu	Asn	Gly	165	170	175
Glu	Ile	Ser	Gln	Leu	Asp	Val	Asp	Gly	Lys	Glu	Ile	Ile	Asn	Glu	Gly	180	185	190
Glu	Val	Phe	Asn	Ser	Tyr	Leu	Leu	Lys	Lys	Val	Thr	Ile	Pro	Thr	Gly	195	200	205
Tyr	Lys	His	Ile	Gly	Gln	Asp	Ala	Phe	Val	Asp	Asn	Lys	Asn	Ile	Ala	210	215	220
Glu	Val	Asn	Leu	Pro	Glu	Ser	Leu	Glu	Thr	Ile	Ser	Asp	Tyr	Ala	Phe	225	230	235
Ala	His	Leu	Ala	Leu	Lys	Gln	Ile	Asp	Leu	Pro	Asp	Asn	Leu	Lys	Ala	245	250	255
Ile	Gly	Glu	Leu	Ala	Phe	Phe	Asp	Asn	Gln	Ile	Thr	Gly	Lys	Leu	Ser	260	265	270
Leu	Pro	Arg	Gln	Leu	Met	Arg	Leu	Ala	Glu	Arg	Ala	Phe	Lys	Ser	Asn	275	280	285
His	Ile	Lys	Thr	Ile	Glu	Phe	Arg	Gly	Asn	Ser	Leu	Lys	Val	Ile	Gly	290	295	300
Glu	Ala	Ser	Phe	Gln	Asp	Asn	Asp	Leu	Ser	Gln	Leu	Met	Leu	Pro	Asp	305	310	315
Gly	Leu	Glu	Lys	Ile	Glu	Ser	Glu	Ala	Phe	Thr	Gly	Asn	Pro	Gly	Asp	325	330	335
Asp	His	Tyr	Asn	Asn	Arg	Val	Val	Leu	Trp	Thr	Lys	Ser	Gly	Lys	Asn	340	345	350

Pro	Tyr	Gly	Leu	Ala	Thr	Glu	Asn	Thr	Tyr	Val	Asn	Pro	Asp	Lys	Ser	355	360	365
Leu	Trp	Gln	Glu	Ser	Pro	Glu	Ile	Asp	Tyr	Thr	Lys	Trp	Leu	Glu	Glu	370	375	380
Asp	Phe	Thr	Tyr	Gln	Lys	Asn	Ser	Val	Thr	Gly	Phe	Ser	Asn	Lys	Gly	385	390	395
Leu	Gln	Lys	Val	Lys	Arg	Asn	Lys	Asn	Leu	Glu	Ile	Pro	Lys	Gln	His	405	410	415
Asn	Gly	Val	Thr	Ile	Thr	Glu	Ile	Gly	Asp	Asn	Ala	Phe	Arg	Asn	Val	420	425	430
Asp	Phe	Gln	Asn	Lys	Thr	Leu	Arg	Lys	Tyr	Asp	Leu	Glu	Glu	Val	Lys	435	440	445
Leu	Pro	Ser	Thr	Ile	Arg	Lys	Ile	Gly	Ala	Phe	Ala	Phe	Gln	Ser	Asn	450	455	460
Asn	Leu	Lys	Ser	Phe	Glu	Ala	Ser	Asp	Asp	Leu	Glu	Glu	Ile	Lys	Glu	465	470	475
Gly	Ala	Phe	Met	Asn	Asn	Arg	Ile	Glu	Thr	Leu	Glu	Leu	Lys	Asp	Lys	485	490	495
Leu	Val	Thr	Ile	Gly	Asp	Ala	Ala	Phe	His	Ile	Asn	His	Ile	Tyr	Ala	500	505	510
Ile	Val	Leu	Pro	Glu	Ser	Val	Gln	Glu	Ile	Gly	Arg	Ser	Ala	Phe	Arg	515	520	525
Gln	Asn	Gly	Ala	Asn	Asn	Leu	Ile	Phe	Met	Gly	Ser	Lys	Val	Lys	Thr	530	535	540
Leu	Gly	Glu	Met	Ala	Phe	Leu	Ser	Asn	Arg	Leu	Glu	His	Leu	Asp	Leu	545	550	555
Ser	Glu	Gln	Lys	Gln	Leu	Thr	Glu	Ile	Pro	Val	Gln	Ala	Phe	Ser	Asp	565	570	575
Asn	Ala	Leu	Lys	Glu	Val	Leu	Leu	Pro	Ala	Ser	Leu	Lys	Thr	Ile	Arg	580	585	590
Glu	Glu	Ala	Phe	Lys	Lys	Asn	His	Leu	Lys	Gln	Leu	Glu	Val	Ala	Ser	595	600	605
Ala	Leu	Ser	His	Ile	Ala	Phe	Asn	Ala	Leu	Asp	Asp	Asn	Asp	Gly	Asp	610	615	620
Glu	Gln	Phe	Asp	Asn	Lys	Val	Val	Val	Lys	Thr	His	His	Asn	Ser	Tyr	625	630	635
Ala	Leu	Ala	Asp	Gly	Glu	His	Phe	Ile	Val	Asp	Pro	Asp	Lys	Leu	Ser	645	650	655

Ser	Thr	Met	Ile	Asp	Leu	Glu	Lys	Ile	Leu	Lys	Leu	Ile	Glu	Gly	Leu	
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Asp	Tyr	Ser	Thr	Leu	Arg	Gln	Thr	Thr	Gln	Thr	Gln	Phe	Arg	Asp	Met	
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Thr	Thr	Ala	Gly	Lys	Ala	Leu	Leu	Ser	Lys	Ser	Asn	Leu	Arg	Gln	Gly	
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Glu	Lys	Gln	Lys	Phe	Leu	Gln	Glu	Ala	Gln	Phe	Phe	Leu	Gly	Arg	Val	
705					710					715					720	
Asp	Leu	Asp	Lys	Ala	Ile	Ala	Lys	Ala	Glu	Lys	Ala	Leu	Val	Thr	Lys	
				725					730					735		
Lys	Ala	Thr	Lys	Asn	Gly	Gln	Leu	Leu	Glu	Arg	Ser	Ile	Asn	Lys	Ala	
			740					745					750			
Val	Leu	Ala	Tyr	Asn	Asn	Ser	Ala	Ile	Lys	Lys	Ala	Asn	Val	Lys	Arg	
		755					760					765				
Leu	Glu	Lys	Glu	Leu	Asp	Leu	Leu	Thr	Gly	Leu	Val	Glu	Gly	Lys	Gly	
	770					775					780					
Pro	Leu	Ala	Gln	Ala	Thr	Met	Val	Gln	Gly	Val	Tyr	Leu	Leu	Lys	Thr	
785					790					795					800	
Pro	Leu	Pro	Leu	Pro	Glu	Tyr	Tyr	Ile	Gly	Leu	Asn	Val	Tyr	Phe	Asp	
				805					810					815		
Lys	Ser	Gly	Lys	Leu	Ile	Tyr	Ala	Leu	Asp	Met	Ser	Asp	Thr	Ile	Gly	
			820					825					830			
Glu	Gly	Gln	Lys	Asp	Ala	Tyr	Gly	Asn	Pro	Ile	Leu	Asn	Val	Asp	Glu	
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Asp	Asn	Glu	Gly	Tyr	His	Ala	Leu	Ala	Val	Ala	Thr	Leu	Ala	Asp	Tyr	
	850					855					860					
Glu	Gly	Leu	Asp	Ile	Lys	Thr	Ile	Leu	Asn	Ser	Lys	Leu	Ser	Gln	Leu	
865					870					875					880	
Thr	Ser	Ile	Arg	Gln	Val	Pro	Thr	Ala	Ala	Tyr	His	Arg	Ala	Gly	Ile	
				885					890					895		
Phe	Gln	Ala	Ile	Gln	Asn	Ala	Ala	Ala	Glu	Ala	Glu	Gln	Leu	Leu	Pro	
			900					905					910			
Lys	Pro	Gly	Met	His	Ser	Glu	Lys	Ser	Ser	Ser	Ser	Glu	Ser	Ala	Asn	
		915					920					925				
Ser	Lys	Asp	Arg	Gly	Leu	Gln	Ser	His	Pro	Lys	Thr	Asn	Arg	Gly	Arg	
	930					935					940					
His	Ser	Ala	Ile	Leu	Pro	Arg	Thr	Gly	Ser	Lys	Gly	Ser	Phe	Val	Tyr	
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Asn	Glu	Thr 35	Ser	Gly	Pro	Val	Asp 40	Asp	Thr	Val	Thr	Asp 45	Leu	Phe	Ser
Asp	Lys 50	Arg	Thr	Thr	Pro	Glu 55	Lys	Ile	Lys	Asp	Asn 60	Leu	Ala	Lys	Gly
Pro 65	Arg	Glu	Gln	Glu	Leu 70	Lys	Ala	Val	Thr	Glu 75	Asn	Thr	Glu	Ser	Glu 80
Lys	Gln	Ile	Thr	Ser 85	Gly	Ser	Gln	Leu	Glu 90	Gln	Ser	Lys	Glu	Ser 95	Leu
Ser	Leu	Asn 100	Lys	Thr	Val	Pro	Ser	Thr 105	Ser	Asn	Trp	Glu	Ile 110	Cys	Asp
Phe	Ile	Thr 115	Lys	Gly	Asn	Thr	Leu 120	Val	Gly	Leu	Ser	Lys 125	Ser	Gly	Val
Glu	Lys 130	Leu	Ser	Gln	Thr	Asp 135	His	Leu	Val	Leu	Pro 140	Ser	Gln	Ala	Ala
Asp 145	Gly	Thr	Gln	Leu 150	Ile	Gln	Val	Ala	Ser	Phe 155	Ala	Phe	Thr	Pro	Asp 160
Lys	Lys	Thr	Ala	Ile 165	Ala	Glu	Tyr	Thr	Ser 170	Arg	Ala	Gly	Glu	Asn 175	Gly
Glu	Ile	Ser 180	Gln	Leu	Asp	Val	Asp	Gly 185	Lys	Glu	Ile	Ile	Asn 190	Glu	Gly
Glu	Val	Phe 195	Asn	Ser	Tyr	Leu	Leu 200	Lys	Lys	Val	Thr	Ile 205	Pro	Thr	Gly
Tyr 210	Lys	His	Ile	Gly	Gln	Asp 215	Ala	Phe	Val	Asp	Asn 220	Lys	Asn	Ile	Ala
Glu 225	Val	Asn	Leu	Pro	Glu 230	Ser	Leu	Glu	Thr	Ile 235	Ser	Asp	Tyr	Ala	Phe 240
Ala	His	Leu	Ala	Leu 245	Lys	Gln	Ile	Asp	Leu 250	Pro	Asp	Asn	Leu	Lys 255	Ala

Ile	Gly	Glu	Leu	Ala	Phe	Phe	Asp	Asn	Gln	Ile	Thr	Gly	Lys	Leu	Ser	260	265	270
Leu	Pro	Arg	Gln	Leu	Met	Arg	Leu	Ala	Glu	Arg	Ala	Phe	Lys	Ser	Asn	275	280	285
His	Ile	Lys	Thr	Ile	Glu	Phe	Arg	Gly	Asn	Ser	Leu	Lys	Val	Ile	Gly	290	295	300
Glu	Ala	Ser	Phe	Gln	Asp	Asn	Asp	Leu	Ser	Gln	Leu	Met	Leu	Pro	Asp	305	310	315
Gly	Leu	Glu	Lys	Ile	Glu	Ser	Glu	Ala	Phe	Thr	Gly	Asn	Pro	Gly	Asp	325	330	335
Asp	His	Tyr	Asn	Asn	Arg	Val	Val	Leu	Trp	Thr	Lys	Ser	Gly	Lys	Asn	340	345	350
Pro	Ser	Gly	Leu	Ala	Thr	Glu	Asn	Thr	Tyr	Val	Asn	Pro	Asp	Lys	Ser	355	360	365
Leu	Trp	Gln	Glu	Ser	Pro	Glu	Ile	Asp	Tyr	Thr	Lys	Trp	Leu	Glu	Glu	370	375	380
Asp	Phe	Thr	Tyr	Gln	Lys	Asn	Ser	Val	Thr	Gly	Phe	Ser	Asn	Lys	Gly	385	390	395
Leu	Gln	Lys	Val	Lys	Arg	Asn	Lys	Asn	Leu	Glu	Ile	Pro	Lys	Gln	His	405	410	415
Asn	Gly	Val	Thr	Ile	Thr	Glu	Ile	Gly	Asp	Asn	Ala	Phe	Arg	Asn	Val	420	425	430
Asp	Phe	Gln	Asn	Lys	Thr	Leu	Arg	Lys	Tyr	Asp	Leu	Glu	Glu	Val	Lys	435	440	445
Leu	Pro	Ser	Thr	Ile	Arg	Lys	Ile	Gly	Ala	Phe	Ala	Phe	Gln	Ser	Asn	450	455	460
Asn	Leu	Lys	Ser	Phe	Glu	Ala	Ser	Asp	Asp	Leu	Glu	Glu	Ile	Lys	Glu	465	470	475
Gly	Ala	Phe	Met	Asn	Asn	Arg	Ile	Glu	Thr	Leu	Glu	Leu	Lys	Asp	Lys	485	490	495
Leu	Val	Thr	Ile	Gly	Asp	Ala	Ala	Phe	His	Ile	Asn	His	Ile	Tyr	Ala	500	505	510
Ile	Val	Leu	Pro	Glu	Ser	Val	Gln	Glu	Ile	Gly	Arg	Ser	Ala	Phe	Arg	515	520	525
Gln	Asn	Gly	Ala	Asn	Asn	Leu	Ile	Phe	Met	Gly	Ser	Lys	Val	Lys	Thr	530	535	540
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Ser	Glu	Gln	Lys	Gln	Leu	Thr	Glu	Ile	Pro	Val	Gln	Ala	Phe	Ser	Asp	
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Asn	Ala	Leu	Lys	Glu	Val	Leu	Leu	Pro	Ala	Ser	Leu	Lys	Thr	Ile	Arg	
			580					585					590			
Glu	Glu	Ala	Phe	Lys	Lys	Asn	His	Leu	Lys	Gln	Leu	Glu	Val	Ala	Ser	
		595					600					605				
Ala	Leu	Ser	His	Ile	Ala	Phe	Asn	Ala	Leu	Asp	Asp	Asn	Asp	Gly	Asp	
	610					615					620					
Glu	Gln	Phe	Asp	Asn	Lys	Val	Val	Val	Lys	Thr	His	His	Asn	Ser	Tyr	
625					630					635					640	
Ala	Leu	Ala	Asp	Gly	Glu	His	Phe	Ile	Val	Asp	Pro	Asp	Lys	Leu	Ser	
				645					650					655		
Ser	Thr	Ile	Val	Asp	Leu	Glu	Lys	Ile	Leu	Lys	Leu	Ile	Glu	Gly	Leu	
			660					665					670			
Asp	Tyr	Ser	Thr	Leu	Arg	Gln	Thr	Thr	Gln	Thr	Gln	Phe	Arg	Asp	Met	
		675					680					685				
Thr	Thr	Ala	Gly	Lys	Ala	Leu	Leu	Ser	Lys	Ser	Asn	Leu	Arg	Gln	Gly	
	690					695					700					
Glu	Lys	Gln	Lys	Phe	Leu	Gln	Glu	Ala	Gln	Phe	Phe	Leu	Gly	Arg	Val	
705					710					715					720	
Asp	Leu	Asp	Lys	Ala	Ile	Ala	Lys	Ala	Glu	Lys	Ala	Leu	Val	Thr	Lys	
				725					730					735		
Lys	Ala	Thr	Lys	Asn	Gly	Gln	Leu	Leu	Glu	Arg	Ser	Ile	Asn	Lys	Ala	
			740					745					750			
Val	Leu	Ala	Tyr	Asn	Asn	Ser	Ala	Ile	Lys	Lys	Ala	Asn	Val	Lys	Arg	
	755						760					765				
Leu	Glu	Lys	Glu	Leu	Asp	Leu	Leu	Thr	Gly	Leu	Val	Glu	Gly	Lys	Gly	
	770					775					780					
Pro	Leu	Ala	Gln	Ala	Thr	Met	Val	Gln	Gly	Val	Tyr	Leu	Leu	Lys	Thr	
785					790					795					800	
Pro	Leu	Pro	Leu	Pro	Glu	Tyr	Tyr	Ile	Gly	Leu	Asn	Val	Tyr	Phe	Asp	
				805					810					815		
Lys	Ser	Gly	Lys	Leu	Ile	Tyr	Ala	Leu	Asp	Met	Ser	Asp	Thr	Ile	Gly	
			820					825					830			
Glu	Gly	Gln	Lys	Asp	Ala	Tyr	Gly	Asn	Pro	Ile	Leu	Asn	Val	Asp	Glu	
		835					840					845				
Asp	Asn	Glu	Gly	Tyr	His	Ala	Leu	Ala	Val	Ala	Thr	Leu	Ala	Asp	Tyr	
	850					855					860					

Glu Gly Leu Asp Ile Lys Thr Ile Leu Asn Ser Lys Leu Ser Gln Leu
 865 870 875 880
 Thr Ser Ile Arg Gln Val Pro Thr Ala Ala Tyr His Arg Ala Gly Ile
 885 890 895
 Phe Gln Ala Ile Gln Asn Ala Ala Ala Glu Ala Glu Gln Leu Leu Pro
 900 905 910
 Lys Pro Gly Thr His Ser Glu Lys Ser Ser Ser Ser Glu Ser Ala Asn
 915 920 925
 Ser Lys Asp Arg Gly Leu Gln Ser Asn Pro Lys Thr Asn Arg Gly Arg
 930 935 940
 His Ser Ala Ile Leu Pro Arg Thr Gly Ser Lys Gly Ser Phe Val Tyr
 945 950 955 960
 Gly Ile Leu Gly Tyr Thr Ser Val Ala Leu Leu
 965 970

<210> 8

<211> 969

<212> PRT

<213> Streptococcus pyogenes

<400> 8

Val Lys Glu Pro Ile Leu Lys Gln Thr Gln Ala Ser Ser Ser Ile Ser
 1 5 10 15
 Gly Ala Asp Tyr Ala Glu Ser Ser Gly Lys Ser Lys Leu Lys Ile Asn
 20 25 30
 Glu Thr Ser Gly Pro Val Asp Asp Thr Val Thr Asp Leu Phe Ser Asp
 35 40 45
 Lys Arg Thr Thr Pro Glu Lys Ile Lys Asp Asn Leu Ala Lys Gly Pro
 50 55 60
 Arg Glu Gln Glu Leu Lys Ala Val Thr Glu Asn Thr Glu Ser Glu Lys
 65 70 75 80
 Gln Ile Asn Ser Gly Ser Gln Leu Glu Gln Ser Lys Glu Ser Leu Ser
 85 90 95
 Leu Asn Lys Arg Val Pro Ser Thr Ser Asn Trp Glu Ile Cys Asp Phe
 100 105 110
 Ile Thr Lys Gly Asn Thr Leu Val Gly Leu Ser Lys Ser Gly Val Glu
 115 120 125
 Lys Leu Ser Gln Thr Asp His Leu Val Leu Pro Ser Gln Ala Ala Asp
 130 135 140
 Gly Thr Gln Leu Ile Gln Val Ala Ser Phe Ala Phe Thr Pro Asp Lys
 145 150 155 160

Lys	Thr	Ala	Ile	Ala	Glu	Tyr	Thr	Ser	Arg	Ala	Gly	Glu	Asn	Gly	Glu	165	170	175	
Ile	Ser	Gln	Leu	Asp	Val	Asp	Gly	Lys	Glu	Ile	Ile	Asn	Glu	Gly	Glu	180	185	190	
Val	Phe	Asn	Ser	Tyr	Leu	Leu	Lys	Lys	Val	Thr	Ile	Pro	Thr	Gly	Tyr	195	200	205	
Lys	His	Ile	Gly	Gln	Asp	Ala	Phe	Val	Asp	Asn	Lys	Asn	Ile	Ala	Glu	210	215	220	
Val	Asn	Leu	Pro	Glu	Ser	Leu	Glu	Thr	Ile	Ser	Asp	Tyr	Ala	Phe	Ala	225	230	235	240
His	Leu	Ala	Leu	Lys	Gln	Ile	Asp	Leu	Pro	Asp	Asn	Leu	Lys	Ala	Ile	245	250	255	
Gly	Glu	Leu	Ala	Phe	Phe	Asp	Asn	Gln	Ile	Thr	Gly	Lys	Leu	Ser	Leu	260	265	270	
Pro	Arg	Gln	Leu	Met	Arg	Leu	Ala	Glu	Arg	Ala	Phe	Lys	Ser	Asn	His	275	280	285	
Ile	Lys	Thr	Ile	Glu	Phe	Arg	Gly	Asn	Ser	Leu	Lys	Val	Ile	Gly	Glu	290	295	300	
Ala	Ser	Phe	Gln	Asp	Asn	Asp	Leu	Ser	Gln	Leu	Met	Leu	Pro	Asp	Gly	305	310	315	320
Leu	Glu	Lys	Ile	Glu	Ser	Glu	Ala	Phe	Thr	Gly	Asn	Pro	Gly	Asp	Asp	325	330	335	
His	Tyr	Asn	Asn	Arg	Val	Val	Leu	Trp	Thr	Lys	Ser	Gly	Lys	Asn	Pro	340	345	350	
Tyr	Gly	Leu	Ala	Thr	Glu	Asn	Thr	Tyr	Val	Asn	Pro	Asp	Lys	Ser	Leu	355	360	365	
Trp	Gln	Glu	Ser	Pro	Glu	Ile	Asp	Tyr	Thr	Lys	Trp	Leu	Glu	Glu	Asp	370	375	380	
Phe	Thr	Tyr	Gln	Lys	Asn	Ser	Val	Thr	Gly	Phe	Ser	Ser	Lys	Gly	Leu	385	390	395	400
Gln	Lys	Val	Lys	Arg	Asn	Lys	Asn	Leu	Glu	Ile	Pro	Lys	Gln	His	Asn	405	410	415	
Gly	Val	Thr	Ile	Thr	Glu	Ile	Gly	Asp	Asn	Ala	Phe	Arg	Asn	Val	Asp	420	425	430	
Phe	Gln	Asn	Lys	Thr	Leu	Arg	Lys	Tyr	Asp	Leu	Glu	Glu	Val	Lys	Leu	435	440	445	
Pro	Ser	Thr	Ile	Arg	Lys	Ile	Gly	Ala	Phe	Ala	Phe	Gln	Ser	Asn	Asn	450	455	460	

Leu	Lys	Ser	Phe	Glu	Ala	Ser	Asp	Asp	Leu	Glu	Glu	Ile	Lys	Glu	Gly	465	470	475	480
Ala	Phe	Met	Asn	Asn	Arg	Ile	Glu	Thr	Leu	Glu	Leu	Lys	Asp	Lys	Leu	485	490	495	
Val	Thr	Ile	Gly	Asp	Ala	Ala	Phe	His	Ile	Asn	His	Ile	Tyr	Ala	Ile	500	505	510	
Val	Leu	Pro	Glu	Ser	Val	Gln	Glu	Ile	Gly	Arg	Ser	Ala	Phe	Arg	Gln	515	520	525	
Asn	Gly	Ala	Asn	Asn	Leu	Ile	Phe	Met	Gly	Ser	Lys	Val	Lys	Thr	Leu	530	535	540	
Gly	Glu	Met	Ala	Phe	Leu	Ser	Asn	Arg	Leu	Glu	His	Leu	Asp	Leu	Ser	545	550	555	560
Glu	Gln	Lys	Gln	Leu	Thr	Glu	Ile	Pro	Val	Gln	Ala	Phe	Ser	Asp	Asn	565	570	575	
Ala	Leu	Lys	Glu	Val	Leu	Leu	Pro	Ala	Ser	Leu	Lys	Thr	Ile	Arg	Glu	580	585	590	
Glu	Ala	Phe	Lys	Lys	Asn	His	Leu	Lys	Gln	Leu	Glu	Val	Ala	Ser	Ala	595	600	605	
Leu	Ser	His	Ile	Ala	Phe	Asn	Ala	Leu	Asp	Asp	Asn	Asp	Gly	Asp	Glu	610	615	620	
Gln	Phe	Asp	Asn	Lys	Val	Val	Val	Lys	Thr	His	His	Asn	Ser	Tyr	Ala	625	630	635	640
Leu	Ala	Asp	Gly	Glu	His	Phe	Ile	Val	Asp	Pro	Asp	Lys	Leu	Ser	Ser	645	650	655	
Thr	Ile	Val	Asp	Leu	Glu	Lys	Ile	Leu	Lys	Leu	Ile	Glu	Gly	Leu	Asp	660	665	670	
Tyr	Ser	Thr	Leu	Arg	Gln	Thr	Thr	Gln	Thr	Gln	Phe	Arg	Asp	Met	Thr	675	680	685	
Thr	Ala	Gly	Lys	Ala	Leu	Leu	Ser	Lys	Ser	Asn	Leu	Arg	Gln	Gly	Glu	690	695	700	
Lys	Gln	Lys	Phe	Leu	Gln	Glu	Ala	Gln	Phe	Phe	Leu	Gly	Arg	Val	Asp	705	710	715	720
Leu	Asp	Lys	Ala	Ile	Ala	Lys	Ala	Glu	Lys	Ala	Leu	Val	Thr	Lys	Lys	725	730	735	
Ala	Thr	Lys	Asn	Gly	Gln	Leu	Leu	Glu	Arg	Ser	Ile	Asn	Lys	Ala	Val	740	745	750	
Leu	Ala	Tyr	Asn	Asn	Ser	Ala	Ile	Lys	Lys	Ala	Asn	Val	Lys	Arg	Leu	755	760	765	

Glu Lys Glu Leu Asp Leu Leu Thr Gly Leu Val Glu Gly Lys Gly Pro
 770 775 780
 Leu Ala Gln Ala Thr Met Val Gln Gly Val Tyr Leu Leu Lys Thr Pro
 785 790 795 800
 Leu Pro Leu Pro Glu Tyr Tyr Ile Gly Leu Asn Val Tyr Phe Asp Lys
 805 810 815
 Ser Gly Lys Leu Ile Tyr Ala Leu Asp Met Ser Asp Thr Ile Gly Glu
 820 825 830
 Gly Gln Lys Asp Ala Tyr Gly Asn Pro Ile Leu Asn Val Asp Glu Asp
 835 840 845
 Asn Glu Gly Tyr His Ala Leu Ala Val Ala Thr Leu Ala Asp Tyr Glu
 850 855 860
 Gly Leu Asp Ile Lys Thr Ile Leu Asn Ser Lys Leu Ser Gln Leu Thr
 865 870 875 880
 Ser Ile Arg Gln Val Pro Thr Ala Ala Tyr His Arg Ala Gly Ile Phe
 885 890 895
 Gln Ala Ile Gln Asn Ala Ala Ala Glu Ala Glu Gln Leu Leu Pro Lys
 900 905 910
 Pro Gly Thr His Ser Glu Lys Ser Ser Ser Ser Glu Ser Ala Asn Ser
 915 920 925
 Lys Asp Arg Gly Leu Gln Ser Asn Pro Lys Thr Asn Arg Gly Arg His
 930 935 940
 Ser Ala Ile Leu Pro Arg Thr Gly Ser Lys Gly Ser Phe Val Tyr Gly
 945 950 955 960
 Ile Leu Gly Tyr Thr Ser Val Ala Leu
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<210> 9

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 9

gtagtcaccc accatatgga agtttttag

29

<210> 10

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 10

ttttttcttt gcggccgcag ttattagt

28

<210> 11

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 11

ggggatccca cccacaatca gg

22

<210> 12

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 12

ggttgtcgac agtaaagcaa cgctagtg

28

<210> 13

<211> 21

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Signal peptide

<400> 13

Met Lys Lys His Leu Lys Thr Val Ala Leu Thr Leu Thr Thr Val Ser
1 5 10 15

Val Val Thr His Asn

20

<210> 14

<211> 6

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Anchoring motif

<220>

<221> MOD_RES

<222> (3)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (6)
<223> Any amino acid

<400> 14
Leu Pro Xaa Thr Gly Xaa
1 5